OM of US-09-525-998A-1 ... A_Genseq_1101 ... ... set_format : pfs

Date: Apr 23, 2002 10:13 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL=frame-n2p.model -DEV-xlp
-Q=... ... -DB-A_Genseq_1101 -QFMT=fasta -SUFFIX=A_rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCT=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.650 -XGAPOP=10.000 -XGAPEXT=0.500
-EGAPOP=6.000 -EGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT-7.000 -START=1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST=45 -LOCALIGN-200 -THR_SCORE-pct
-THR_MAX-100 -THR_MIN=0 -ALIGN-15 -MODE=LOCAL -OUTFMT=pfs
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Search information block:
Query: US-09-525-998A-1
Query length: 1368
Database: A_Genseq_1101:*
Database sequences: 522463
Database length: 740/73290
Search time (sec): 140.140000

seq_documentation_block:
ID   AAR10986 standard; Protein; 455 AA.
XX
AC   AAR10986;
XX
DT   13-MAY-1991 (first entry)
XX
DE   30kD TNF inhibitor precursor.
XX
KW   Tumour necrosis factor, inhibitor.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Cleavage-site   40..41
FT   note=" cleavage gives active protein "
XX
PN   AU9058976-A.
XX
PD   24-JAN-1991.
XX
PF   16-JUL-1990;   9GAU-0058976.
PR   07-FEB-1990;   9G9S-0479661.
PP   18-JUL-1990;   9G9S-0381080.
FF   11-DEC-1989;   9G9S 0453229.
XX
IA   (5LNo.) SINAGEN NC.
XX

alignment_scores:
Length: 455
Gaps: 0
Percent identity: 100.000

alignment_block:

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34  euGlyAspArgGlnLysArgAspSerValCysProGlnGlyGlyLysTyrIle  50

151 CACCCTCAAAATAATTCGATTTGTCTGCTACCAAGTCCCACAAAGGAACCTA 200
    ||||||||||||||||||||||||||||||||||||||||||||||||
51  HisProGluAsnAsnSerIleCysCysSerThrLysCysSerHisSerLysGlyThrTyr 67

201 CTTGTACAATGACTGTCCAGCCCCAGGGCCAGGATACGGACTGCAGGGAGT 250
    ||||||||||||||||||||||||||||||||||||||||||||||||
67  rLeuTyrAsnAspCysSerProGlyProGlnTyrGlnAspThrAspCysSerGluC 84

251 GTGAGGAGCGGCTCGTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 300
    ||||||||||||||||||||||||||||||||||||||||||||||||
84  ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100

301 AGCTGCTCCAAATGCCGAAAGAAATGGGTCAGGTGGACATCTTCTTTG 350
    |||||||||||||||||||||||||||||||||||||||||||||
101 SerCysSerSerLysCysSerAsnGluValGluLeuSerSerCy 117

351 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCAGTACCGGC 400
    ||||||||||||||||||||||||||||||||||||||||||||||||
117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134

401 ATTATTGGAGTGAAAACCTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 450
    ||||||||||||||||||||||||||||||||||||||||||||||
134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150

451 AATGGGACCGTGCACCTCTCCGCCAGGAGAAACAGAACACCCTGCCAC 500
    ||||||||||||||||||||||||||||||||||||||||||||||
151 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 167

501 CTGCCATGCAGGTTCTTCTAAGAAAAGAGTGTGTCCCTGTAGTA 550
    |||||||||||||||||||||||||||||||||||||||||||
167 rCysHisAlaGlyPhePheLysArgGluAsnGluCysValSerCysSerA 184

551 ACTGTAAGAAAAGCCTGGAATGCACCAAGTTGTGCCTACCCCAGATTGAG 600
    ||||||||||||||||||||||||||||||||||||||||||||||
184 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200

601 AAATGTAAGCCTAAGGCTGGGAGTCCCACCACACATGTGGTGCCCCCGCT 650
    ||||||||||||||||||||||||||||||||||||||||||||||||
201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuVa 217

651 CATTTCTTGGTGTTGCCTTTATCCCTCCTTCATTGGTTTAATGT 700
    ||||||||||||||||||||||||||||||||||||||||||
217 lIlePhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMet 234

701 ATCCTACAACAGCGTGGAAGTCCAAGCTCACTCCATTGTTTGTGGGAAA 750
    ||||||||||||||||||||||||||||||||||||||||||||||||
234 YrArgTyrGlnArgTrpLysSerLysLeuTyrSerIleValCysGlyLys 250

751 TCGACACTTCAAAAAGAGAGCGGAGCTTCAAGCAACTACTAAGGCCCT 800
    ||||||||||||||||||||||||||||||||||||||||||||||
251 SerThrProGlyTyrGluGlyGluCysThrArgThrLysLysProLysCa 267

801 GGCCCAACCCAAGCTTCCAGTCCCATTCGGCCCCCACCCTGG 850
    ||||||||||||||||||||||||||||||||||||||||
267 GAlaGlnAsnProSerPheProSerProGlyPheThrProLeuG 284

851 GCTTCCAGTCCGGTCCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 900
    ||||||||||||||||||||||||||||||||||||||||||||||||
284 yrPheProSerProValProSerSerThrPheThrSerSerThrTyrThr 300

901 CCCGGTGACTGTCCCAACTTCGGGGCTCCCCGCAGACAGGTGGCACCACC 950
    ||||||||||||||||||||||||||||||||||||||||||||||||
301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPr 317

951 CTATCAGGGCGGGGTGACCCCATGTTGGACAGCCGTGCTCCGACCCCA 1000
    ||||||||||||||||||||||||||||||||||||||||||||||
317 oTyrGlnGlyGlyValThrLeuProValThrAlaLeuGlyArgLeuAspP 334
```

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1001 TCCCCAACCCCTTCAGAAGTGGGAGGACAGCAGCCCCAACCCACAGAGC 1050
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334  leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer 350

1051 CTAGACACTGATGACCCCGCGAGCTGTAGCGCGTGGTGGAAAGTGCC 1100
     |||||||||||||||||||||||||||||||||||||||||||||||
351  LeuAspThrAspAspProAlaThrLeuTyrAlaValAlaGluAsnValPr 367

1101 CCCGTTGCCTGGAAGAAATTCGTGCGCGTGCCTTAGGGCTGAGrGACCACG 1150
     ||||||||||||||||||||||||||||||||||||||||||||||||
367  oProLeuArgTrpLysGlnPheValArgArgLeuGlyLeuSerAspHisG 384

1151 AGATCGATCGGCTGCAGCGTGCAGAACGGGCGGCCGCCTGGGCGAGGCGCAA 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||
384  luIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400

1201 TACAGCATGCTGGCGACCTGGAGCGGCGAGGCGAGGCGGGGGAGGGCGAC 1250
     ||||||||||||||||||||||||||||||||||||||||||||||||
401  TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaTh 417

1251 GCTGGAGTTGCTGGGAGCGGTGGCTCGCGGATGGACCTGCTGGGCTGCC 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||
417  rLeuGluLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysL 434

1301 TCGGAGGACATCGAGGAGGCGCTTTCGCGGCCCGCCTTCCGCCCCCG 1350
     |||||||||||||||||||||||||||||||||||||||||||||
434  euGluAspIleGluGluAlaLeuCysGlyProAlaProProAla 450

1351 CCCAGTCTTCTCAGA 1365
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451  ProSerLeuLeuArg 455
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seq_name: /SIDS2/gcqdata/geneseq/geneseq/AA1993.DAT:AAR42059

XX
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX
PS   Disclosure; Page 57-59; 85pp; English.
XX
CC   The sequences given in AAR42058-59 represent human tumour necrosis
CC   factor receptor (TNF-R) and the sequences in AAR42060-61 represent
CC   human interleukin-1 receptor (IL-1R). These sequences were used in
CC   the production of a fusion protein which conformed to one of the
CC   formulae:
CC   TNF-R-linker-TNF-R-linker-IL-1R
CC   IL-1R-linker-TNF-R-linker-TNF-R or
CC   TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala. These linkers separate the individual moieties
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity. These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role. They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
XX
SQ   Sequence   455 AA;

alignment_scores:
            Quality: 2497.00   Length: 455
              Ratio: 5.466   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAR42059

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      |||||||||||||||||||||||||||||||||||||||
   51 HisProIlnAsnAsnSerTleCysCysThrLysCysHisLysLysSerValThr 67

  201 CTTGTACAATCACTGTCCAGAGGCGGGGCGAGGATACGGACATCTAGGGAG 250
      |||||||||||||||||||||||||||||||||||||||
   67 rLeuTyrAsnAspCysSerProGlyProGlnGlnAspThrAspCysArgGluC 84

  251 GTGAGAGGGCTCTTCAGCGGTTCAGAAAACACCTCAGACACTGGCTC 300
      |||||||||||||||||||||||||||||||||||||||
   84 ysGluSerGlySerPheThrValLeuSerGluAsnHisSerLeuArgHisCysVal 100

  301 AGCTGGTCCAAATGCCGAAAGAAATGGGTCAGGTGGAGATCTCTTCCTTG 350
      |||||||||||||||||||||||||||||||||||||||
  101 SerCysSerLysCysArgLysGluMetGlyValTleLeuSerSerC 117

  351 CACACTGGACCCGGACACCGGTGTGCTGCGCTGCAGAAGAACCAGTAGCCGGC 400
      |||||||||||||||||||||||||||||||||||||||
  117 sThrValAspArgAspThrValCysArgCysArgGlyGluLysAspGlnTyrArgH 134

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               ||||||||||||||||||||||||||||||||||||||||||||
     434 euGluAspT11eGluCysGlyProSerGlyProSerGlyProSerGlyProAlaAlaLeuProProAla 450
     1451 CCCAGTCTTCTCAGA 1365
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     451 ProSerLeuLeuArg 455

seq_name: /US-US2/qrqpqtq/qpqpqseq/qpqpseq/qpqpseq/IE-/AA1qq5-qAT-/AA7qnqA

seq_documentation_block.
ID   AAR75084 standard; Protein; 455 AA.
XX
AC   AAR75084;
XX
DT   19-JAN-1996  (first entry)
XX
DE   p55 TNF-R.
XX
KW   p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera,
KW   epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW   phorbol myristate acetate; PMA.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH
FT   Peptide         41..53
FT                   /note= "N terminus of soluble p55 TNF-R"
FT   Modified site   54..56
FT                   /note= "glycosylation site"
FT   Modified site   145..147
FT                   /note= "glycosylation site"
FT   Modified site   161..163
FT                   /note= "glycosylation site"
FT   Peptide         193..210
FT                   /note= "peptide used in creation of chimeras"
FT   Region          198..210
FT                   /note= "spacer region"
FT   Misc-difference 201
FT   Misc-difference 202
FT                   /note= "major C terminus for soluble p55 TNF-R"
FT                   /note= "essential for shedding reaction'
FT   Misc-difference 203
FT                   /note= "minor C terminus for soluble p55 TNF-R"
FT   Region          212..234
FT                   /note= "transmembrane region"
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RN   AD947574?-A.
XX
PD   04-MAY-1995.
XX
PF   11-OCT-1994;   94AD-0075742.
XX
PR   12-OCT-1993;   93IL-0107268.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Balkin M.  Brakebusch C,  Vartolomeev E,  Wallach D;
XX
DR   WPI; 1995-194342/26.
DR   N PSDB, AAC90513.
XX
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
XX
PS   Disclosure; Fig 1; 40pp; English.
XX
CC   This sequence represents human p55 tumour necrosis factor (TNF-R).
CC   Expression of this receptor is regulated by shedding of the
CC   extracellular receptor fragment. The p55 TNF-R can be shed in response
CC   to different inducing agents, e.g. phorbol myristate acetate (PMA),
CC   depending on cell type. The only region of the receptor whose structure
CC   affects the shedding response is the spacer region (see AAR75012) in the
```

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CC   extracellular domain  This region is located close to a site of cleavage
CC   of the molecule, and links the Cys rich module to the transmembrane
CC   domain. The spacer region of the encoded protein was used to create the
CC   chimeras between human p55 TNF-R and murine epidermal growth factor
CC   receptor (EGF-R) that are represented by AAR75007-11. This spacer region
CC   was subjected to deletion mutations (AAR75013-25) and substitutions
CC   (AAR75026, 47)  of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gln 175  with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173.  Mutations which alter the
CC   conformation of the protein adversely affect the shedding process.
CC   The mutations shown in AAR75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R.  Fragments of these inhibitors can be seen in
CC   AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3.  These protease
CC   inhibitors can be used for enhancing TNF function.
XX
SQ   Sequence   455 AA;

alignment_scores:
     Quality:  2487.00              Length:    455
     Ratio:   5.466                 Gaps:        0
Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAR75084

Align seg 1/1 to: AAR75084  from: 1  to: 455

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51  GCTCTTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGCCCTCACC  100
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17  uLeuLeuValGlyGlyAsnIleProLeuArgGlyLeuLeuAspTrpPro  34

101 TAGGGACAGGGAGAAGATATGTGTGTCGAGAAAAGGAAATATATC  150
    |||||||||||||||||||||||||||||||||||||||||||||
34  euGlyAspArgGluGlyLysArgAspSerValCysValGlnLysLys  50

151 CAGGGTCAAAATAATGGATTGTGTACCAACGGCACGAAAGGAAGCTA  200
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51  HisProGlnAsnAsnSerIleCysCysThrLysGlyThrLysSerSer  67

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251 GTGAGGGCTGTTTCAGGGTTCTGGAAAAGCACCTCAGACACTGCGCTC  300
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84  ysGluSerGlySerPheThrAlaSerGluSerHisSerAspThrCysLeu  100

301 AGCTGCTCCAAATGCCGAAAGAAATGGCTCAGGTGGCATCTCTTCCTG  350
    ||||||||||||||||||||||||||||||||||||||||||||||||
101 SerCysSerLysCysArgLysTrpMetGlyGlnValGluSerSerCys  117

351 CACACTGGAGGGGCACAACGGGTCTGGCGTGCGCAGGAAGAACCAGTAGGGC  400
    |||||||||||||||||||||||||||||||||||||||||||||||||||||
117 sThrValAspAlaGlyAspThrValCysGlyCysArgLysAsnGlnTyrArgH  134

401 ATFATGGAGGAAAACCTTTCCAGTGGTTCAATTGCAAGCTCTGGCTC  450
    ||||||||||||||||||||||||||||||||||||||||||||||||
134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  150

451 AAGGGGATCCATGGACAGTCTGGTCCTAAGAAGAAAACAGAACACCGTGCGGAC  500
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
151 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysThr  167

501 CTGCCATGCAGGTTGTTTCTAAGCAGAGAAAACGAGTGGCTGCTGTAGTA  550
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ID   AAY30944 standard; Protein; 455 AA.
XX
AC   AAY30944;
XX
DT   18-OCT-1999  (first entry)
XX
DE   Human tumour necrosis factor binding protein.
XX
KW   Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW   anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW   autoimmune glomerulonephritis; cerebral malaria; immune response;
KW   antagonist; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /label= signal_peptide
FT   Protein         30..455
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FT                   /note= "hypothetical glycosylation site"
FT   Region          213..230
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FT   Modified-site   250
FT                   /note= "hypothetical glycosylation site"
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PD   01-SEP-1999.
XX
PF   11-AUG-1998;  98DE 9116707.
XX
PR   20-APR-1990;  89CH-0001347.
PR   12-SEP-1989;  89CH-0003319.
PR   08-MAR-1990;  89CH 0950746.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M, Lesmiis Z, Gentz R, Lesslauer W, Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 1999-480840/41.
DR   N-PSDB; AAY09170.
XX
PT   New insoluble proteins, and fragments, that bind to e.mol necrosis
PT   factor, used to treat e.g. septic shock or cerebral malaria
XX
PS   Claim 4a; Fig 1; 25pp; German.
XX
CC   This invention describes novel homogeneous insoluble proteins (1),
CC   their (insoluble) trimers (1a) and their salts that can bind tumour
CC   necrosis factor (TNF). The products of the invention have
CC   anti-inflammatory and antimalarial activity. (i) and (ia) are used (i)
CC   to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC   glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC   (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC   diagnostic application of TNF in body fluids. Antibodies raised against
CC   (1) are used to purify protein (1a) and (1). This sequence represents
CC   a tumour necrosis factor binding protein, described in the method of
CC   the invention.
XX
SQ   Sequence  455 AA;

alignment_scores:
   Quality:  2487.00          Length:  455
   Ratio:    5.466            Gaps:    0
   Percent Similarity: 100.000   Percent Identity: 100.000
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167 ArgCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184
551 ACTGTAAGCAAAAGCCTGGAGTCCAGGACTGCCAAGTTGTGCCTACCCCAGCATTGAG 600
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184 SerCysLysGlnLysProGlySerGlnAspCysArgLeuCysAlaProGlyHisGlu 200
601 AATGTTAAGGGCACTGAGGACTGAGCACCACAGTGTGTTGCCCCTGGT 650
    |||||||||||||||||||||||||||||||||||||||||||
201 AsnValLysGlyThrGluAspCysArgLysTyrThrValLeuGluCysThrGlyCysVa 217
651 CATTTTCTTTGGTCTTGCCTTTATCCCCTCTTTATCCCCTCTCTC 700
    ||||||||||||||||||||||||||||||||||||||||
217 HisPheGlyLeuAlaLeuSerLeuArgLeuIleGlyLeuMetT 234
701 ATGGCTACCAACCGTGGAAGTCCAAGTCTACTCCATTGTTGTGGGAAA 750
    |||||||||||||||||||||||||||||||||||||||||
234 TyrArgTyrGlnArgTrpLysSerGlyLysLeuTyrSerIleCysGlyLys 250
751 TCGACACCTGAAAAAAGGGGGAGTTGAAGGAACTACTACTAAGCCCT 800
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251 SerThrProGlySerLysTrpGlnGlnTrpThrThrLysLysProLeu 267
801 CGCCCAAACCCAAGCTCACTGGCCACTGCAGCGTTCACCCCCACCCTTG 850
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267 ArgAlaProAsnProSerSerPheSerProTrpGlyTrpPheThrProThrLeuG 284
851 GCTTCAGTCCGTGCCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 900
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284 LysPheSerProValProSerThrThrPheThrTyrSerSerSerThrThrTyrThr 300
901 CCCAGTGAGTGGCCAATTTGGTGGACAGCAG 950
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301 ProGlyAspCysSerProAsnPheAlaAlaProArgArgArgGluArgValAlaProThr 317
951 CTATCAGGGAGGCGAGACCATCCTGGCAGACGGGCTGGAGCTCGGCCGGAGCCCCA 1000
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317 TyrTyrArgGlyAlaAsnProIleLeuAlaThrAlaLeuAlaSerAspArgProI 334
1001 TCCCCAACCCCTCAGAAGTGGGAGAGGACGACCGGGCCCCACAAGGCCACAGAGC 1050
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334 LeuProAsnProLeuGlnLysTrpGluGluAspAspArgAlaHisLysAlaThrGluSer 350
1051 CTAGCACTGATGACCCGCAGTGTTATCCGTGTTAGTGAGCAG 1100
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351 LeuAspAspArgGlnCysTyrProValSerTrpArgAsnValPr 367
1101 CCCGTTGCGGTGAAGAGGAATCTGCTGCGGCCCTAGGGCTGAGCCGACACC 1150
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367 ProLeuArgTrpLysSerProValArgArgArgGlyTrpProAla 384
1151 ACAGCCATGGCCTGGAGCTGCAGAACGGGACTCGGGACAGCGGAGGGCAA 1200
     ||||||||||||||||||||||||||||||||||||||||||
384 GlnAlaAspThrAlaTrpSerLeuGlnAsnGlyThrArgCysSerLeuArgGluAlaGln 400
1201 TACAGCATGTGGAAGATTGGAGAAGCAAGAGCAGCAGCAATA 1250
     |||||||||||||||||||||||||||||||||||||
400 TyrSerMetLeuAlaThrTrpProAlaArgArgGlyArgThrAlaGluAlaThr 417
1251 GGTGGAGCTGCTGGGAGCCGGTCCTGGGCCATCGGAGCTGCGGC 1300
     ||||||||||||||||||||||||||||||||||||||||
417 ArgLeuLeuGlyLeuArgValLeuAsnArgAspMetLysPheLeuLeuGlyCysSerL 434
1301 TCCAGGACATCGAGGAGCGGCTTGGTGCGGCCGCGCCTGCGGCCGGCGCG 1350
     ||||||||||||||||||||||||||||||||||||||||||
434 GluLeuAspPheIleGluGluArgLeuArgTyrSerGlyProAlaAlaGluProProAla 450
1351 CCCAGTCTTCTCAGA 1365
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450 ProSerLeuLeuArg 455
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seq_name: us-09-525-998a-1.rag   AAY30944

seq_documentation_block:

alignment_block:
US 09-525-998A-1 x AAY10934   ..

Align seq 1/1   to: AAY10934   from: 1   to: 455

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    1 MetGlyLeuGlnThrValProAspLeuLeuLeuProLeuValLeuLeuGl  17

   51 GCTGTTGGTGGGAATATACCTTTAGGGTTATTAGGACTGGTCCTCACC  100
      ||||||||||||||||||||||||||||||||||||||||||||||
   17 uLeuLeuValGlyIleTyrTyrProSerGlyValIleGlyLeuValProHisL  34

  101 TAGGGACACGGGACAAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATC  150
      ||||||||||||||||||||||||||||||||||||||||||||||
   34 euGlyAspArgGluLysArgAspSerValCysProGlnGlyLysTyrIle  50

  151 CACCCTCAAAATAATTCGATTTGCTGCTACCAACGTGCCACAAAGGAACCTA  200
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   51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy  67

  201 CTTGTACAATGACTGTCCAGGCCAGAGGAATAACGGACTGCAGGGAGT  250
      ||||||||||||||||||||||||||||||||||||||||||||||
   67 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC  84

  251 GTGAGAGGCGGCTCTTCAGCGGTTCAGAAAACCACTCAGACACTGCCTC  300
      ||||||||||||||||||||||||||||||||||||||||||||||
   84 ysGluGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu  100

  301 AGCTGCTCCAAATGCCGAAAGGGAAATCGGTCATTGGAGATATTCTTTTG  350
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  101 SerCysSerLysCysArgLysGlyGlnGluGlyGlnValLysGlnSerSerCy  117

  351 CACATTGGACCGGGAACACGTGTGGAGGTGCAGAAGAAGAAAGCAGTACCGGC  400
      ||||||||||||||||||||||||||||||||||||||||||||||
  117 sThrValAspArgAspThrValCysGlyCysLysSerGlnHisTyrArgH  134

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      ||||||||||||||||||||||||||||||||||||||||||||||
  134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  150

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  151 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh  167

  501 CTGCTCATGGAGGTTCTTTCTAAGAGAAAATCAGTGTGTTTCTGTAGTA  550
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  167 rCysHisAlaGlyPheProLeuArgGluAsnGlnCysValSerCysSerA  184

  551 ACTGTAAGAGAAGAGGCGAGTTTGGAGGACACCTACCCAGATTGAG  600
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  184 snCysLysGlySerLeuGlyCysSerThrLysSerLeuProGluIleIle  200

  601 AAGTGTAAGGGCAGGACACTCAGGACCAGTGCTGTTCCCCCGGT  650
      ||||||||||||||||||||||||||||||||||||||||||||||
  201 AsnValLysGlyThrArgGlnAspSerCysThrThrValLeuLeuProLeuVa  217

  651 CATTTTCTTGTCCTTGGCTTTTATCCCTCGTTTCATTGGTTTAATGT  700
      ||||||||||||||||||||||||||||||||||||||||||||||
  217 lIlePheLeuGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetT  234

  701 ATCGGTACCAACGGTGGAAGTGCGAAGTCCATGCTACTGCATTGTTGTGGGGAAA  750
      ||||||||||||||||||||||||||||||||||||||||||||||
  234 yrArgTyrGlnArgTrpLysSerLysLeuTyrSerIleValCysGlyLys  250

  751 TCGACACCTAAACCCTGAAAAAGAGGGCAGCTTCAAGCAACTACTAAGACCCCT  800
      ||||||||||||||||||||||||||||||||||||||||||||||
  250 SerThrProLysProGluLysGluGlyGlySerPheLysGlnThrLysSerProL  267

  801 GGCCCTAAACGCAAGTTCAGTGACATCCCACCAGGTTCACCCCACGATACCGG  850
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  267 GlyAlaProAsnProSerPheSerProThrProGlyPheThrProThrLeuG  284
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  851 GCTTCAGTCCCGTGCCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC  900
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  284 lyPheSerProValProSerSerThrPhePheThrSerSerThrTyrThr  300

  901 CCCGGTGATGTTCCAATTTGGGGCCCGGAGAAAGTTGCACGACC  950
      ||||||||||||||||||||||||||||||||||||||||||||||
  301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProT  317

  951 CTATCAGGGGCTGACCCCATCCTTGCGAGAGCCCTCGCCTCGACCCCA  1000
      ||||||||||||||||||||||||||||||||||||||||||||||
  317 oTyrGlnGlyAlaAspProIleLeuAlaArgLeuGlySerAspProI  334

 1001 TCCCAACCCCCTTCCAGAGAACTGGGAGGACAGCGGCCACAGCACCAGC  1050
      ||||||||||||||||||||||||||||||||||||||||||||||
  334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer  350

 1051 CTTACTACTTAGAACCGGACGTTGTAGGCTGTAGCGGTGGAGAACGTACC  1100
      ||||||||||||||||||||||||||||||||||||||||||||||
  351 LeuAspThrAspProAlaThrLeuTyrAlaValValGluAsnValPrt  367

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  367 oProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisG  384

 1151 AGATCGATCCCCGAGCTGCAGAACGGCCTCGCCTGCCAGGCGGCCAA  1200
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  384 luIleAspProGluLeuGlnGlnAsnGlyArgCysLeuArgGluAlaGln  400

 1201 TACGCATGGTGGAGAATGGAAGGCGGCCACGGGCCGGGGCGGAGGCGAC  1250
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  401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh  417

 1251 GCTGGAGCTGCTGGAGCGGGTGCTCCGGGACATGAACGGTGGCTGGGCTGCC  1300
      ||||||||||||||||||||||||||||||||||||||||||||||
  417 rLeuGluLeuLeuGluArgValLeuArgAspMetAsnGlyLeuGlyCysL  434

 1301 TGGAGGACATCCAGGAGGCTTTTCGAGGGGCGGGGGCGGGGGCCGGG  1350
      ||||||||||||||||||||||||||||||||||||||||||||||
  434 euGluAspIleGluGluLeuCysGlyProAlaAlaLeuProProAla  450

 1351 CCCAGTCTCTCAGA  1365
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  451 ProSerLeuLeuArg  455
```

PA (NIJJ) NIJJ
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P.J.
PA (DIXI/) DIXIT V M

XX
PI Yu G, N J, Gentz RL, Dillon PJ, Dixit VM;
XX
DR WPI: 2000 6872 3/67.
XX
PT Treating graft versus host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PI Containing Receptor proteins and a second therapeutic agent -
XX
PS Disclosure; Fig 3; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial sclerosis diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 455 AA,

alignment_scores:
        Quality: 2487.00   Length: 455
          Ratio: 5.466   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAB36266

Align seq 1/1 to: AAB36266 from: 1 to: 455

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      ||||||||||||||||||||||||||||||||||||||||||||||||||
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  201 CTTGTACAATGACTGTCCAGGCCCGGGCCAGGATACGGACTGCAGGGAGT 250
      |||||||||||||||||||||||||||||||||||||||||||||||||
   67 ThrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 84

  251 GTGAGAGGGGTCGCTTCACAGCTTCCAAAAACCACCTCAGACACTGCCTC  300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
   84 ysGluSerGlySerGlyPheThrAlaSerGlnAsnHisLeuArgHisCysSerL 100

  301 AGTGCTCCCAAATGCCAAAGAAATGAAATGTCAGGTGGAGATCTCTTCTTG 350
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  100 SerCysSerProAsnAlaLysGluMetGlyArgValGluIleSerSerCys  117

  351 CACAGTGACCGGGACACCGGTGTGTCTGCAGGAAGAACCAGTACCCGGC   400
      |||||||||||||||||||||||||||||||||||||||||||||||||
  117 ThrValThrGlyArgAspThrGlyCysSerAlaGlyArgThrSerThrArgH 134

  401 ATTATTGGAGTGAAAACCTTTTCCAGTCGTCAATTGCAGGCTCTGCCTC   450
      |||||||||||||||||||||||||||||||||||||||||||||||||
  134 IleIleGlyValLysThrPheSerSerArgGlnLeuGlnAlaLeuProLeu 150
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1351 CCCAGCTTTCTCAGA 1365
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 451 ProSerLeuLeuArg 455

seq_name: "US5_" prote.n coding protein; AA.5z7 7A: AAB47800
seq_documentation_block:
 ID   AAB47800 standard; protein; 455 AA.
 XX
 AC   AAB47800;
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 DT   23-FEB-2001 (first entry)
 XX
 DE   Human tumour necrosis factor p55 receptor.
 XX
 KW   Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
 KW   p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
 KW   immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
 KW   neutroprotective; respiratory inflammation; infection; Crohn's disease;
 KW   multiple sclerosis; autoimmune disorder; cardiovascular disorder;
 KW   chronic myelogenous leukaemia; inflammation; bowel disease.
 XX
 OS   Homo sapiens.
 XX
 PN   WO200064479-A1.
 XX
 PD   02-NOV-2000.
 XX
 PF   26-APR-2000; 2000WO-US317760.
 XX
 PR   27-APR-1999; 999US-0301274.
 XX
 PA   (ANTI-) ANTIBODY SYSTEMS INC.
 XX
 PI   Fredeking TM; Ignatyev GM;
 XX
 DR   WPI; 2000-679646/66.
 XX
 PT   Novel compositions comprising tetracycline or tetracycline-like
 PT   compositions and methods containing tetracycline or tetracycline-like
 PT   compounds for treating and/or preventing acute inflammatory responses and
 PT   diseases. Such diseases include acute inflammatory conditions associated
 PT   with viral haemorrhagic diseases (including diseases caused by
 PT   colitis -
 PS   Disclosure: Page 167-169; 183pp; English.
 XX
 CC   The present sequence is given in a specification relating to novel
 CC   compositions and methods containing tetracycline or tetracycline-like
 CC   compounds for treating and/or preventing acute inflammatory responses and
 CC   diseases. Such diseases include acute inflammatory conditions associated
 CC   with viral haemorrhagic diseases (including diseases caused by
 CC   Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
 CC   parasitic diseases; bacterial infections, sepsis, cachexia, autoimmune
 CC   disorders, acute cardiovascular events, chronic myelogenous leukaemia and
 CC   transplanted bone marrow-induced graft-versus-host disease, septic shock,
 CC   immune complex-induced colitis, cerebrospinal fluid inflammation,
 CC   multiple sclerosis, inflammatory responses associated with trauma,
 CC   systemic inflammatory response syndrome (SIRS), adult respiratory
 CC   distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
 CC   and Crohn's disease.
 XX
 SQ   Sequence  455 AA;

alignment_scores:
     Quality:  2487.00          Length:   455
     Ratio:     5.466             Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-525-998A-1 x AAB47800
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  51 ................ 100
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  17 uLeuLeuValGlyLlcTyrProSerGlyValIlcGlyLeuValProHisLeu 34

 101 IAGGGGATAGGGAGAGAGAATAGTGTGTCCACAAGGAAAATATATC 150
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  34 euGlyAspArgGluGlySerValCysPheGlnGlyLysTyrIle 50

 151 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTCCCAAAGGAACCTA 200
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  51 HisProGlnAsnAsnSerIleCysCysThrLysSerHisLysGlyThrTy 67

 201 CTTGTACTATGACTGTCVAGCCCAGGAGAGGATACGGATGAGGGAGT 250
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  67 rLeuTyrAspAspCysProCysProGlnAspThrAspCysSerArgCluC 84

 251 GTGAGAGGGCTCCTCACGGTTCAGAAAACCACCTCAGAGAGTGCCTC 300
     ||||||||||||||||||||||||||||||||||||||||||||||
  84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100

 301 AGCTGCTGCAAATGCCGAAAGCAAATGGGTCAGGTGGGAGATCTCTTG 350
     ||||||||||||||||||||||||||||||||||||||||||||||
 101 SerCysCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCy 117

 351 CACAATGGATGGACATCTGTGGAGTCCAGGAAGAACCAGTACCGGC 400
     ||||||||||||||||||||||||||||||||||||||||||||||
 117 sThrValAspAspAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134

 401 ATTATTGGAGTGAAAACCTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 450
     ||||||||||||||||||||||||||||||||||||||||||||||
 134 IsTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150

 451 AATGGCACCGTGCACTCCTCGCCAGGAGAGAAACACAGACCACCGTGCAC 500
     ||||||||||||||||||||||||||||||||||||||||||||||
 151 AsnGlyThrValHisLeuSerCysSerGluLysGlnAsnThrValCysTh 167

 501 CTGCCATGCAGGTTCTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 550
     ||||||||||||||||||||||||||||||||||||||||||||||
 167 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 184

 551 ACTGTAAGAAAAGCTGGAGTGCACGAAGTTGTGCCTACCCAGATTGAG 600
     ||||||||||||||||||||||||||||||||||||||||||||||
 184 snCysLysLysSerTrpSerValHisGluValCysLeuProGlnIleGlu 200

 601 AATGTTAAGGGCCACTGAGGACACACAGGGCTGTTGCCCGTGGT 650
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 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuVa 217

 651 CATTTCTTTGGTCTTTATCCTGTCTTCATTGGTTTAATGT 700
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 217 lHisPhePheGlyLeuCysLeuCysSerLeuLeuPheLleGlyLeuMetT 234

 701 ATCGGTACCAACGGTGGAATCCAAGTCTTACTCCATTGTTGTGGAAA 750
     ||||||||||||||||||||||||||||||||||||||||||||||
 234 yrArgThrProGlnArgTrpLysSerCysLeuTyrSerIleValCysGlyLys 250

 751 TCGACACCTGAAAAAGAGGGGAGCTTCAAGGAACTACTACTAAGCCCCT 800
     ||||||||||||||||||||||||||||||||||||||||||||||
 251 SerThrProGlnLysGlyGluLeuGlyGlyThrProThrCysProLe 267

 801 GGCCCCAAACCAAGTTCAGTCCCCACTCCAGGCTTCACCCCACCCTGG 850
     ||||||||||||||||||||||||||||||||||||||||||||||
 267 gAlaProAsnProSerPheSerProThrGlyPheThrProThrLcaG 284

 851 GCTTCAGTCCCGTGCCCAGTTCACCTTCCACCTTCAGCTCCACCTATACC 900
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 284 lyProSerProValProSerSerThrPheThrProSerProThrTyrThr 300

 901 CCCGTGACTGTCCCAACTTGCGGCTCCACCTGGCACCACC 950
```

PI Ni J, Gentz RL, Yu G, Fan P.
XX
DR WPI; 2000-594575/56.
XX
PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer -
XX
PS Disclosure; Fig 2; 226pp; English.
XX
CC The present sequence is TNFR 1, a member of the tumour necrosis factor
CC receptor family. A novel human tumour necrosis factor receptor,
CC designated TR9, has been isolated. The TR9 receptor is also known as
CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
CC agonists are useful for treating, preventing or diagnosing common
CC variable immunodeficiency, X-linked agammaglobulinaemia, severe combined
CC immunodeficiency, and Wiskott-Aldrich syndrome, autoimmune diseases (such
CC as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,
CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
CC cardiovascular diseases and other neurological diseases.
XX
SO Sequence   455 AA;

alignment_scores:
          Quality: 2487.00   Length: 455
          Ratio: 5.465   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAB26984

Align.seq 1/1 to AAB26984 from: 1 to: 455

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   51 GCTGTTACTGAAAGCAGTGCAATGCAGGTACGTCATGAC........... ....   1..
      |||||||||||||||||||||||||||||||||||||||
   17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyIleValProHisL   34

  101 TAGGGGACAGGGGAGGAGAGAGAGAGAATATGTGTGTGTCCCCAAGAAAAATATATG 150
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   34 euGlyAspArgGlyLysArgAspSerValCysProGlnGlyLysTyrIle   50

  151 CACCCTGAAAATAATTCGATTTGTTAGCAAGTGCCAAAAGAACCTA 200
      ||||||||||||||||||||||||||||||||||||||||||||||
   51 HisProGluAsnAsnSerIleCysCysSerThrLysCysHisLysGlyThrIy   67

  201 CTTGGACAATGAGCTGGACCCCAGGGGCCGGAGGACAGCAGCGAGCAGT 250
      ||||||||||||||||||||||||||||||||||||||||||||||||
   67 rLeuLysAspAsnTyrSerGluSerThrArgAspSerAlaAspLysThrArgH   84

  251 GTGAAGAAAGCTTAGAAAACTAGAAAAAAAAACTGCCTC 300
      |||||||||||||||||||||||||||||||||||||||
   84 ysAspAspAspPheThrAlaSerGluAspHisLeuArgHisCysLeu   100

  301 AGCTGTGTAAATGGGGAAAGGGAAAGGGTCAGTGGAAGAATCTTCTTG 350
      ||||||||||||||||||||||||||||||||||||||||||||||||
  101 SerCysSerGlyCysArgLysCysLysCysGlyValSerSerSerC 117

  351 CACAGTGGAGGGGACACCGTGTGGCGGCTGCAGGAAGAAGAACACAACCGGGC 400
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
  117 SThrValAspArgAspThrValCysGlyValCysSerArgLysAsnGlnTyrArgH   134

  401 ATTATTGAGTGAGAAACCTTTCCAGTGTTCAALLGACGTCTGCCTC 450
      ||||||||||||||||||||||||||||||||||||||||||||||
  134 isTyrTyrProGluAsnLeuPheCysIrCysArrLeuCysTysLeu   150

  451 AATGGGGACGGTGCACCTCCCTGCCAGGAGAAACAAGAACATACGGTGTGCAC 500
      ||||||||||||||||||||||||||||||||||||||||||||||||||||

  301 PISGlyAspPheAlaProPheArgArgGluAlaProAlaPror 317
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 1001 TCCCAAGCCCTTCAGAAGGTGGAGAGCAACAGCCACAAGCACACAGAGC 1050
      ||||||||||||||||||||||||||||||||||||||||||||||||
  334 leProAsnProLeuGlnLysValGluAspSerAlaHisLysHisProGlnSer 350
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 1051 CTAGACACTATGACGGGAGCCGAGCATGATGCGTCATGTGAAGAATGTGACTGAC 1100
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  351 LeuAspThrAspArgProAlaThrLeuTyrAlaValValGlyAsnAsnValPr 367
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 1101 CCCGTCGGCCAAGCAATCCTCACGGCCTACGACATCCCCAGCCAGCATGGCAGTAACG 1150
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  367 oProLeuAlaGlyProL.SerValArgArgLeuGlyLeuSerAspHisGlyG 384
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1151 AGATCGATCAGGCTGAAGTCGACAACAATAAGAGCACGGAGCACAA 1200
      ||||||||||||||||||||||||||||||||||||||||||||||
  384 luGluAspAspLeuGluGlnAsnGlyAsnGlyArgCysLeuArgGluArgGluAlaGln 400
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 1201 TACAGCATGCTGGAGAGCGCGGAGGAGGAGGCCGACCCGCGGGAGGCCAC 1250
      ||||||||||||||||||||||||||||||||||||||||||||||||
  401 TyrSerMetLeuAlaThrTrpArgArgArgArgThrProArgArgArgGluAlaTh 417
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1251 GCTGGAGGCTGCTGGACAGCGCGCCCGGGGACAACCTTGCTGGGGCTGCC 1300
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  417 rLeuGluLeuGlyArgValLeuArgArgAspMetAspLeuLeuGlyCysL 434
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1301 TGGAGAAGATGGAGAAAGATTTGAAGCGGACCACGGAGGGGGACGACGCC 1350
      ||||||||||||||||||||||||||||||||||||||||||||||||||
  434 euGluAspAspLeuGluGlnAsnGlyAsnGlyArgCysGluCysGlyProCysAlaAlaLeuProProAla 450
      ||||||||||||||||||||||||||||||||||||||||||||||||||
 1351 CCCAGTCTTCTCAGA 1365
      |||||||||||||||
  451 ProSerLeuLeuArg 455

seq_name: US-09-525-998A-1 Nucleic acid sequence Seq/AAB26984 v A1 AAB26984
seq_documentation_block:
ID AAB26984 standard; Protein; 455 AA.
XX
AC AAB26984;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human TNFR 1.
XX
KW Human; TNFR 1; tumour necrosis factor; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data.
XX
OS Homo sapiens.
XX
PN WO200056862-A1.
XX
PD 28-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-US06831.
XX
PR 24-MAR-1999; 99US-0126019.
PR 14-MAY-1999; 99US-0134220.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

seq_name: /SIUS2/srqdata/qenreseq/qenreseq11/AAB2000.DAT-AAB23446.

seq_documentation_block:
ID   AAB23446 standard; protein; 455 AA.
XX
AC   AAB23446;
XX
DT   22 JAN 2001 (first entry)
XX
DE   Human tumour necrosis factor receptor 1 protein.
XX
KW   TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW   tumour; cancer; apoptosis; bacterial infection.
XX
OS   Homo sapiens.
XX
PN   WO200050436-A1.
XX
PD   31-AUG-2000.
XX
PF   23-FEB-2000; 2000WO-US04606.
XX
PR   23-FEB-1999; 99US-0121314.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (NAND/) NANDABALAN K.
PA   (SCHU/) SCHULZ V P.
PA   (STEP/) STEPHENS J C.
PA   (CHEW/) CHEW A.
XX
PI   Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX
DR   WPI; 2000-543909/49.
DP   N PSDB; AAA95105.
XX
PT   Polynucleotides comprising polymorphic variants of a reference sequence
PT   for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
PT   biological function of TNFR1 and identifying drugs targeting the
PT   protein for treating disorders -
XX
PS   Claim 10; Fig 5; 79pp; English.
XX
CC   The present invention relates to polymorphic variants of the tumour
CC   necrosis factor receptor 1 (TNFR1) gene. The present sequence is
CC   the TNFR1 protein. The sequence of the whole gene is given in AAA95102,
CC   AAA95103 and AAA95104. The polymorphisms were identified by amplifying
CC   and sequencing regions of the gene. Twelve polymorphic loci
CC   were discovered. Of these twelve polymorphisms, four can cause a
CC   change in the TNFR1 protein. The TNFR1 polymorphisms may be useful
CC   for studying the biological function of TNFR1 as well as for
CC   identifying drugs targeting the protein for treatment of disorders
CC   related to its abnormal expression or function such as tumours,
CC   apoptosis related disorders and bacterial infection.
XX
SQ   Sequence 455 AA;

alignment_scores:
      Quality: 2487.00   Length: 455
      Ratio: 5.466   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAB23446   .

Align seq 1/1 to: AAB23446 from: 1 to: 455

     1 AlGGGCTCTACAGTGACCTGAGTGCCATGTCGTCTCTGGA 50
       ||||||||||||||||||||||||||||||||||||||||
     1 MetGlyLeuSerThrValProAspLeuLeuLeuValLeuGl 17

    51 GCTGTTGGGGAACAGACCCTCAGGTAGGCTAGGGCATCACC 100

seq_name: AS0635 1346 bps consensus ... H AAB....A AAB01336

seq_documentation_block:
ID   AAB01336 standard; Protein; 455 AA.
XX
AC   AAB01346;
XX
DT   25 SEP 2000 (first entry)
XX
DE   TNF-R1 death receptor.
XX
KW   DR144, death receptor, apoptosis, programmed cell death; FAS;
KW   TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO200034335-A2.
XX
PD   15 JUN 2000.
XX
PF   09-DEC-1999; 99WO-US26035.
XX
PR   04-DEC-1998; 98US-0205018.
XX
PA   (SCHE) SCHERING CORP.
XX
PI   Leong C, Phillips JH;
XX
PT   Purified or recombinant polypeptide for modulating apoptosis comprises
PT   a sequence which binds to an antibody specific for UL144 or its
PT   fragments
XX
PS   Disclosure, page 65-67, 75pp; English.
XX
CC   A pure or recombinant polypeptide which binds to a polyclonal antibody
CC   specific for the mature UL144 is useful for screening molecules which

CC   block induction of apoptosis or interfere with antiapoptotic activity.
CC   The polypeptide is also useful for modulating apoptosis and useful in
CC   treatment of conditions associated with abnormal physiology or
CC   development, such as cancer or degenerative conditions and/or
CC   regulation of viral infection and replication. At least five
CC   different death receptors are known, which include the CD95
CC   (Fas/APO-1), the TNF receptor 1, TNF receptor apoptosis-mediated
CC   protein (TRAMP), death receptor-6 (DR-6), and TNF-related
CC   apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4
XX
SQ   Sequence   455 AA;

alignment_scores:
       Quality: 2487.00   Length: 455
       Ratio: 5.466   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAB01336

Align seq 1/1 to: AAB01336   from: 1   to: 455

```
   1 A.GGGCGTCCAAGTTGCCTCAGTCTGCCAGTGTGTCGTCCTGGA   50
     |||||||||||||||||||||||||||||||||||||||||||||
   1 MetGlyLeuSerThrValProAspLeuLeuProLeuLeuValLeuLeuGlu   17

  51 GCTGTTGGTGGGAATATACCCCTCAGGGTTATTGGATGTGGTCCTCACC  100
     |||||||||||||||||||||||||||||||||||||||||||||||||
  17 uLeuLeuValGlyGlyIleTyrProSerGlyValIleGlyValIleProHisL   34

 101 TAGGGGACACGGCAGAAGAGAGATAGTGTGTGTGCCCAAGCAAAATATATC  150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
  44 euGlyAspArgGlnLysArgAspSerValCysProGlnGlyLysTyrIle   50

 151 CACCCTCAAAATAATTCCATTTCCTCA ...CACAAAGGAACCTA   200
     |||||||||||||||||||||||||||||||||||||||||||
  51 HisPro...AspCys...HisHisCysHisGlyThrTy   67

 201 CTTGTACAATGACTGTCCAGGGCGGGGATACGGACTGCCAGGGAGT  250
     |||||||||||||||||||||||||||||||||||||||||||||
  67 rLeuTyrAsnAspCysProGlyPr...GlyHisAspThrAspCysArgGlyLeuC   84

 251 GTGAGAGGCGGCTCTTCAACCGCTTCAGAAAACACCCAGACACTGCCTC  300
     ||||||||||||||||||||||||||||||||||||||||||||||||
  84 ysGluSerGlySerPhePheThrAlaSerGluAsnHisLeuArgHisCysLeu  100

 301 AGTCGTCCAAATGCCGAAAGGAAATGGCTCAGGTGGAGATCCTTCTTG  350
     ||||||||||||||||||||||||||||||||||||||||||||||||
 101 SerCysCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerSerCy  117

 451 CACAGTGGTGGACACGCTGGTGGTTGAGATCGTCATGGACCAACTGAATACGGC  400
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 117 sThrValAspArgAspThrValCysCysSerArgLysAsnCh:TyrArgH  134

 401 AATAATGGAGTGGAAAAGCTTTTCAGTGCTTCAATTGCAGCCTCTGCCTC  450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 144 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  150

 451 AATGGAGCCGTGGACCTCCTCCTCCCAGAGAAAACAGAGACACCGTGGCAC  500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 151 AsnGlyThrValHisLeuSerCysSerGlnGlnLysGlnAsnThrValCysTh  167

 551 ACTGTAAGAAAAGGTTGGAGTGGAGGTGGAGCAAGTTGGCTACCCCAGAAGGAG  600
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
 167 rCysHisSerAlaGlyProAspCysArgGluAsnCysVal SerCysSerScrA  184

 601 AATGTTAAGGGCACCAGAGACGCACCACCACCAGGTGTGCCCCTGGT  650
     |||||||||||||||||||||||||||||||||||||||||||||||
 184 snCysGlyLysSerLeuGluLysPro...LeuProAsnGluHisGlu...  200
```

```
291 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuVa  217
651 CATTTTCTTGGTCTTGGCTTTATCCCTCCTTTCATTGGTTTAATGT  700
    |||||||||||||||||||||||||||||||||||||||||||||
217 IlePhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetT  234

701 ATCGGTACCAACGGTGGAAGTCCAAGTCCACTCCATTGTTGTGGGAAA  750
    ||||||||||||||||||||||||||||||||||||||||||||||||
234 yrArgTyrGlnArgTrpLysSerLysSerTyrSerIleValCysGlyLys  250

751 TCGAACCTCAAAAAGAGGGAGTTGAAGGAAT...TATAAGGCCCTA  800
    |||||||||||||||||||||||||||||||||||||||||||||
251 SerThrProGlyLysGluGlyLeuGlyGly...ThrThrHisLysProLeu  267

861 GGGCTCAAAGCAAGTTCAGTCCAACTCAAGGTTCACCCACCGCACCCTGG  850
    ||||||||||||||||||||||||||||||||||||||||||||||||||
267 uAlaProAspProSerPheSerProGln...PheThrProThrLeuG  284

851 GCTTCAGTCCCCTGCCCAGTTCCACCTTCACCCCAGCTCCACCTATACC  900
    |||||||||||||||||||||||||||||||||||||||||||||||||
284 lyPheSerProValProSerSerProThrSerProSerSerSerThrTyrThr  300

901 CCAGGGAGTTTCCCAACTTGGGGTCCCCGGAGGAGAAGAGTGGCACCACC  950
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 ProGlyAspCysProAsnPheAlaAlaProArgArgArgGluValAlaProPr  317

951 CTATCAGGGGCTGACCCATCCTTGGACCGTCCGTCTCAAGATCCACCCCA 1000
    ||||||||||||||||||||||||||||||||||||||||||||||||||
317 oTyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProI  334

1001 TCCCCAACCCCTTCAGAGAGTGGGAGGACAGCGGCCCCAAAGCCACCAGAGC 1050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer  350

1051 CTAGACACTCATGAACCGGAGTGGTAGGAGTGTATGGAGAAGTGCGT 1100
     |||||||||||||||||||||||||||||||||||||||||||||||
351 LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnValPr  367

1101 CCGGTTGAGTGGAAGAATTGGTGAGGGAGGTAGGGTGAGGTGAGGCCACACG 1150
     |||||||||||||||||||||||||||||||||||||||||||||||||
367 oProLeuArgTrpLysGlnPheValArgArgLeuGlyLeuSerAspHisG  384

1151 AGATCCATGGTCGCTCAGCGTGCAGAACGGGCGGCTGCCTCCTGCGAGGGCCAA 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
384 luIleAspArgArgLeuGlnLeuGlnAsnGlyArgCysLeuArgGlnAlaGln  400

1201 TACACGTGTGGGAACTTGGAGGGCTGGGGGAGATCGTCGAGGCCAC 1250
     ||||||||||||||||||||||||||||||||||||||||||||||
401 TyrSerMetLeuAlaThrArgArgArgThrProArgArgGluAlaTh  417

1251 GCTGAGGTGGTGGGAGTGAGATCGACAGTCTGGGCTGCC 1300
     |||||||||||||||||||||||||||||||||||||||
417 rLeuGluLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysL  434

1301 TCGGAGGACATCGGAGGAGGCGGCTTTCGGGGGCGCCCCCGGCG 1350
     ||||||||||||||||||||||||||||||||||||||||||
434 euGluAspIleGluGluAlaLeuCysGlyProAlaAlaLeuProProAla  450

1351 CCCAGTCTTCTCAGA 1365
     |||||||||||||||
451 ProSerLeuLeuArg 455
```

seq_name: /SIDS2/qcgdata/geneseqp/AA2001.DAT:AAB36697

KW   Human; tumour necrosis factor receptor 5, TRID, TNFR-5, TR5, androgen;
KW   TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW   tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW   immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW   anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW   gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW   apoptosis-cell death related disease; autoimmune disorder;
KW   cardiovascular disorder; viral infection.
OS   Homo sapiens.
XX
PN   WO200071150-A1.
XX
PD   30-NOV-2000.
XX
PF   18-MAY-2000; 2000WO-US13515.
XX
PR   20-MAY-1999; 99US-0135164.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Wei Y, Ruben SM, Gentz RL, Ni J;
XX
DR   WPI: 2001-041051/05.
XX
PT   Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT   necrosis factor receptor 5, useful in the diagnosis, treatment or
PT   prevention of cancer, autoimmune disorders and viral infection -
XX
PS   Disclosure: Fig 2; 285pp; English.
XX
CC   The present invention describes the human TRID protein (tumour necrosis
CC   factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC   intracellular domain, also referred to as tumour necrosis factor
CC   receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC   neotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC   antiparasitic, cardiant, anti HIV, antiparkinsonian and vasotropic
CC   activities, and can be used in gene therapy. The TRID polynucleotides
CC   are useful for detecting complementary polynucleotides. TRID proteins and
CC   polynucleotides are useful in the treatment of tumours, resistance to
CC   parasite, bacteria and viruses, restenosis and graft versus host disease.
CC   They are also useful for inducing proliferation of T-cells, endothelial
CC   cells and certain haematopoietic cells, to regulate antiviral responses
CC   and to prevent certain autoimmune diseases after stimulation of TRID by
CC   an agonist of TRAIL binding facilitator. The antibodies which bind TRID
CC   polypeptides are useful for treating and/or preventing diseases
CC   associated with increased or decreased apoptotic cell death. The TRID
CC   polynucleotides, proteins, antibodies, agonists and antagonists are
CC   useful in the diagnosis, treatment or prevention of: (a) cancer;
CC   (b) autoimmune disorders; (c) diseases associated with increased
CC   apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC   present sequence represents a tumour necrosis factor receptor used in
CC   comparison with TRID in the exemplification of the present invention.
XX
SQ   Sequence 455 AA.

alignment_scores:
     Quality: 2487.00   Length: 455
     Ratio: 5.466   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAB36697   .

Align seq 1/1 to: AAB36697 from: 1 to: 455

    1 ATGGGCTCTCCACCGGCCTGAACCTGCTGACTGGTGCTCCTGGA 50
      ||||||||||||||||||||||||||||||||||||||||||||
    1 MetGlyLeuSerThrValProAspLeuLeuProLeuLeuLeuGl 17

   51 GCTGTGCTGGCAATATACCTCACAGGTTATTGAAGTAGGTTAACC 100
      |||||||||||||||||||||||||||||||||||||||||||||
   17 oTyrGlnGlyAlaAspProIleLeuLeuProLeuLeuLeuGl 33

XX
PS   Example 6, Fig 21, 82pp, English.
XX
CC   The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC   (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC   novel TNF inhibitors of the present invention are useful as therapeutic
CC   agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC   for treating inflammatory and degenerative diseases mediated by TNF. The
CC   present sequence is the precursor for 30 kDa TNF inhibitor. The 30 kDa
CC   TNF inhibitor can inhibit TNF alpha.
XX
SQ   Sequence   455 AA;

alignment_scores:
         Quality: 2487.00   Length: 455
         Ratio: 5.466   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-525-998A-1 x AAB37677

Align seq 1/1 to: AAB37677   from: 1 to: 455

    1 ATGGGCCTCTCCACGTGCGTGACCTGTCTGGCACTGGCGTGCCTCCTGGA 50
      ||||||||||||||||||||||||||||||||||||||||||||||||||
    1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuGl 17

   51 GCTGTAGTGGAATATGCCTTAGGAGTTATTGGATTGTGCCTCAC 100
      ||||||||||||||||||||||||||||||||||||||||||||
   17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL 34

  101 TAGGGACAGGGAGAGAGAGATAGTGTGTCCCCAAGAAAATATATC 150
      |||||||||||||||||||||||||||||||||||||||||||||
   34 euGlyAspArgGluLysArgAspSerValCysProGlnLysTyrIle 50

  151 CACCCTCAAAAAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 200
      ||||||||||||||||||||||||||||||||||||||||||||||||
   51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67

  201 CTTGTACAATGACTTCCAGGCGGAGGTAATCGATGAGGGAGT 250
      ||||||||||||||||||||||||||||||||||||||||||
   67 rLeuTyrAsnAspCysProGlyProGlyGluAspValIleAspGluGluC 84

  251 GTGATGGTGTTTCTACCGTTCAGAAAACACTAGACACTGCCTC 300
      |||||||||||||||||||||||||||||||||||||||||||
   84 ysGluSerGlySerPheThrAlaSerPheAsnHisLeuArgHisCysSerLeu 100

  301 AGCTGCTCCAAATGCCCAAAGGAAATGGGTCAGGTGGAGATCTCTTCTG 350
      |||||||||||||||||||||||||||||||||||||||||||||||||
  101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 117

  351 CACAGTGGACCGGGACACATGTGGTGGTTCAGAGAACAGTAGGGA 400
      |||||||||||||||||||||||||||||||||||||||||||||
  117 sThrValAspArgAspThrValCysGlyCysArgGlysAsnGlnTyrArgH 134

  401 ATTATTGGATGAAAACCTTTCCAGTGTTCAATTGAGCCTCTGCCTC 450
      ||||||||||||||||||||||||||||||||||||||||||||||
  134 isTyrTrpSerGluAsnLeuPheGluCysPheAsnCysSerLeuCysLeu 150

  451 AATGAGCCGTGCACCCTGCCACCTTCCCAGGAGAAACAGAACACCGTGTGCAC 500
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
  151 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 167

  501 CTGCTACAGTTCTTTCTAAGAAAACGAGTGTGTCTCGTAGTA 550
      ||||||||||||||||||||||||||||||||||||||||||
  167 rCysHisSerGlyPheCysArgGluAsnGlyCysValSerCysSerA 184

  551 ACTGTAAGAAACTGAGTGACGGAATTGTGTTACCAAATGAG 600
      |||||||||||||||||||||||||||||||||||||||||
  184 snCysLysLysSerLeuSerAspGlyCysThrLysCysLeuProGluIleGlu 200

  601 AAGTTTAAGGGCACTGAAGACATGGGCACCAACAGCGCCCCCGT 650

 1001 TCCCCAACCCCTTCAGAAGGTGGAGACAGACAACAAGCCACAACAGAGC 1050
      |||||||||||||||||||||||||||||||||||||||||||||||||
  334 leProAsnProLeuGlnLysTrpGluAspArgSerAlaHisLysProGlnSer 350

 1051 CTAGACACTGATCACCCCCACCCGACCCCGGTGGGAGACGTGCC 1100
      ||||||||||||||||||||||||||||||||||||||||||||
  351 LeuAspThrAspAspProAlaThrLeuTyrAlaValGluAsnValPr 367

 1101 CCATTGAGGTGGAAATTGTAGGATGAGGACATGGGACTACG 1150
      |||||||||||||||||||||||||||||||||||||||||
  367 aProLeuGluArgTrpLysGluValArgLeuLeuSerAspHisC 384

 1151 AGATCCATCGGTGGATGCCAGAAGTGTGGAGGTGGACGGGAA 1200
      ||||||||||||||||||||||||||||||||||||||||||
  384 luIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400

 1201 TACAGCATGGACGTTGCAGTTGCAGTGGCCAGGCAC 1250
      ||||||||||||||||||||||||||||||||||||
  401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgArgGluAlaTh 417

 1251 GCTGAGCTGCTGGGACGGCGTCTGGACAGTGCTGGCTGCC 1300
      ||||||||||||||||||||||||||||||||||||||||
  417 rLeuGluGluLeuGlyArgValLeuArgValLeueuGlyCysL 434

 1301 TCGAGGACACATCGAGGACGGGCGTTTCCGGGGCCGGCCCGCCGCCG 1350
      |||||||||||||||||||||||||||||||||||||||||||||||
  434 euGluAspIleGluGluAspAlaLeuCysGlyProAlaAlaLeuProProAla 450

 1351 CCCAGTCTCTCAGA 1365
      ||||||||||||||
  451 ProSerLeuLeuArg 455

seq_name: AB1552/gcqdata-genesseq/genesseq-AA.2001 PAT: AAB37677

seq_documentation_block:
ID   AAB37677 standard, protein; 455 AA.
XX
AC   AAB37677;
XX
DT   02-MAR-2001 (first entry)
XX
DE   Human 30 kDa TNF inhibitor precursor.
XX
KW   TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin.
KW   IL-1; inflammatory disease; degenerative disease; human.
XX
OS   Homo sapiens.
XX
PN   US6143866-A.
XX
PD   07-NOV-2000.
XX
PF   19-JAN-1995;   95US-0375242.
XX
PR   19-JUL-1990;   90US-0555274.
PR   09-JUL-1993;   93US-0090366.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
PR   07-FEB-1990;   90US-0479661.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI   Vanderslice RW, Vannice J, Kohno T;
XX
DR   WPI; 2001-008443491
DR   N-PSDB; AAC83946.
XX
PT   Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT   non-native cysteine residue cross linked with polyethylene glycol,
PT   useful for treating inflammatory and degenerative diseases mediated by
PI   TNF -

XX
KW   Tumour Necrosis Factor; binding proteins; heat shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
XX
FH   Key   Location/Qualifiers
FT
FT   Modified-site   54
FT   /label= putative N-glycosylation site
FT   Modified-site   145
FT   /label= putative N-glycosylation site
FT   Modified-site   151
FT   /label= putative N glycosylation site
FT   Modified-site   270
FT   /label= putative N-glycosylation site
FT   Region   217..230
FT   /label= transmembrane region
FT   Peptide   1..28
FT   /label= signal peptide
XX
PN   EP417563-A.
XX
PD   20-MAR-1991.
XX
PF   31-AUG-1990;   90EP-0116707.
XX
PR   20-APR-1990;   90H-0001347.
PR   12-SEP-1989;   89H-0003319.
PR   08-MAR-1990;   90CH-0000746.
XX
PA   (HOFF) HOFFMANN LA ROCHE AG.
XX
PI   Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI   Schlaeger EJ;
XX
DR   WPI; 1991 EP, A12.
DR   N-PSDB; AAQ10955.
XX
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
XX
PS   Claim 1; Fig 1; 26pp; German.
XX
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF BPS (see AAR 1072-E11982), and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment in use as a probe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the DNA encoding
CC   sequence may also contain a fragment encoding a human Ig domain.
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also AAQ10956.
XX
SQ   Sequence   455 AA;

alignment_scores:
           Quality: 4494.00   Length: 455
              Ratio: 9.459   Gaps: 6
Percent Similarity: 100.000   Percent Identity: 99.780

alignment_block:
US-09-525-998A 1 x AAR11082

Align seq 1/1 to: AAR11082 (from: 1 to: 455

    1 ATGGGCCTCTCCACGGTCCGGCTGACCTGGCACCGAGGCGACCTGCCCTCCGGA 54
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
    1 MetGlyLeuSerThrValProLeuThrTrpHisArgGlyAspLeuProSerGly 18

   51 GCTGTGGTGGAGAATAAAGAGGTCAGCGGCCTTGGAGCTGCTGGACTTGGTCAC 100
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
   19 AlaValValGluAsnLysGluValSerGlyLeuGlyProGlyValHisLeuGlu 34

seq_documentation_block:
ID   AAR11082 standard. Protein, 455 AA.
XX
AC   AAR11082;
XX
DT   24-MAY-1991 (first entry)
XX
DE   Human 55kD TNF-binding protein.

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1001 TCCCCAACCCCTTCAAGAAGTGGGAGGACAGCGCCCACAAGCCACACAGC 1050
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer 350

1051 CTAGAACTGATGACCCCAGCTGATAGAGTGGCTGAGAAGAACCTGGC 1100
     |||||||||||||||||||||||||||||||||||||||||||||||
 351 LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnValPr 367

1101 CCGTTGTCTGAAGAATTGGTCTGAGGTCTAGGAGGACCAG 1150
     ||||||||||||||||||||||||||||||||||||||||
 367 oProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisG 384

1151 AGATCCATCGGCTGTGACTGCAGAACCGGCCCACCGCCCAA 1200
     |||||||||||||||||||||||||||||||||||||||||
 384 luIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400

1201 TACAGCATGCTGGCCAATTGGAGCCGTGAGAGGAGGAGGAC 1250
     |||||||||||||||||||||||||||||||||||||||||
 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh 417

1251 GTGAGCTGTGAGTGTGAGAAATAGTGGCTGAGTTGT 1400
     ||||||||||||||||||||||||||||||||||||
 417 rLeuGluLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysL 434

1301 TGGAGGACATCGAGGAGGGGTTTGCGGCCCCCCCCGCCCCG 1350
     |||||||||||||||||||||||||||||||||||||||||
 434 euGluAspIleGluGluAlaLeuCysGlyProAlaAlaLeuProProAla 450

1351 CCCAGTCTTCTCAGA 1365
     |||||||||||||||
 451 ProSerLeuLeuArg 455
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seq_nam_   /SIBS2/q:qdata/q-protseq/q-protseq:AA1992.DAT:AAR20787

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seq_documentation_block:
ID   AAR20787 standard; Protein; 455 AA.
XX
AC   AAR20787;
XX
DT   11-MAY-1992  (first entry)
XX
DE   TNF-alpha binding protein.
XX
KW   Tumour necrosis factor alpha; autoimmune diseases; cachectin;
KW   extracellular domain.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   Peptide          1..40
FT                    /note= "signal peptide"
FT   Peptide          41..455
FT                    /note= "mature peptide"
FT   Domain           30..199
FT                    /note= "extracellular domain"
FT   Domain           212..234
FT                    /note= "transmembrane domain"
FT   Modified-site    145..147
FT                    /note= "potential N-glycosylation site"
FT   Modified-site    151..153
FT                    /note= "potential N-glycosylation site"
XX
PN   GB246569-A.
XX
PD   05-FEB-1992.
XX
PF   15-JUN-1990;  90GB-0013410.
XX
PR   15-JUN-1990;  90GB-0013410.
XX
PA   (CHAP-) CHAIRING CROSS SUNLE.
XX
PI   Feldman M, Gray P, Turner M, Brennan F;
```

```
101 TAGGGGACAGAACAAGAGACATACGTGTGTCCCCAAGCAAAAATATATC 150
    |||||||||||||||||||||||||||||||||||||||||||||||||
 34 euGlyAspArgGluLysArgAspSerValCysProGlnGlyLysTyrIle 50

151 CACCCTTCAAAATAATTCGATTGCTGTACCAAGTGCCACAAAGGAAACCTA 200
    |||||||||||||||||||||||||||||||||||||||||||||||||||
 51 HisProGlnAsnAsnSerIleCysTyrCysTrpLysCysHisLysGlyThrTy 67

201 CTTGTACAATGACTGTCCAGCTGGGAGAGAATACGGACTGCAGGGGAGT 250
    |||||||||||||||||||||||||||||||||||||||||||||||||
 67 rLeuTyrAsnAspCysProGlyProGlyProGlnAspThrAspCysArgGluC 84

251 GTGAGAGCGGCTGCTTCAGCGGTTCAGAAAACCACCACTCAGACACTGCCCTC 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
 84 ysGluSerGlySerPheThrAlaSerGluPheThrAlaSerGluHisHisCysLeu 100

301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGCGTGGAGATCTCTTCTTG 350
    |||||||||||||||||||||||||||||||||||||||||||||||||||
101 SerCysSerCysSerArgLysSerGluMetGlyGlnArgValGluIleSerSerCy 117

351 CACAGTGGATGAGGACACAGTGCTGGTGTAGAAAACCATACGGC 400
    ||||||||||||||||||||||||||||||||||||||||||||
117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134

401 ATTATTGCAGTGAAAACCTTTCCAGTGCCTCAATTGCAGCCTCCGCCTC 450
    |||||||||||||||||||||||||||||||||||||||||||||||||
134 isTyrTrpSerGlyAsnLeuPheGlnCysPheAsnCysSerLeuCysSerLeu 150

451 AATGGCACCTGCACCTCTCCCCAGGACGAAAACAGAACACCGTGTGCAC 500
    |||||||||||||||||||||||||||||||||||||||||||||||||
151 AsnGlyThrValHisLeuCysGlnCysGlnAsnThrValCysTh 167

501 CTGCCATGCAGGTTTCTTCTAAAGAAAACGACTGTGTTTCTGTAGTA 550
    |||||||||||||||||||||||||||||||||||||||||||||||
167 rCysHisAlaGlyPheLeuValArgGluAsnGluCysValSerCysSerSerA 184

551 ACTGTAAGCAAAGCTGGCACGCAGCAGCTTGCGCTAGCCCAGAATTGCAG 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||
184 snCysLysLysSerGluLeuGlnCysThrLysLysLeuFLeuGlnLeuAla 200

601 AATGTTAAGGGCACTGAAGACACTAGAGCATAGTGCGTGTTTGCCCTGCCT 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
200 AsnValLysGlyThrGluAspThrGlyTyrThrThrValLeuLeuProLeuVa 217

651 CATTTTCTTTGGTCTTTGCCTTTTATCCCCTCCTTCATTGGTTTAATGT 700
    |||||||||||||||||||||||||||||||||||||||||||||||||
217 lIlePhePheGlyValCysGlyLeuLeuSerLeuLeuPheIleGlyLeuMetT 234

701 ATGGCTACCAAGCGGCGGAAGTGCCAAGCTCCACTACCCATTGTTTGTGGGAAA 750
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
234 yrArgTyrGlnArgTrpLysSerArgLeuTyrSerIleLeuGlyValCysGlyLys 250

751 TCGACCACCTGAAAAACAGGGGCAGCTTGAAGGAAAACTACTACTAAGCCCCT 800
    |||||||||||||||||||||||||||||||||||||||||||||||||||||
250 SerThrThrProGlyGlyGlnGlyGlnLeuGlyThrThrThrLysSerProLe 267

801 GGCCCCAAACGCAAGTTCAGTTGACATTGCCAGTTCACCCAACCTGG 850
    |||||||||||||||||||||||||||||||||||||||||||||||
267 uAlaProAsnProSerPheSerProThrProGlyPhePheProThrLeuG 284

851 GCTTCAGTCGCCGTGCCCAGTTCACCTTCAACTTCCAGCTCCAACTATACC 900
    |||||||||||||||||||||||||||||||||||||||||||||||||||
284 lyPheSerProValProSerSerThrPheThrSerSerSerTyrTyrThr 300

901 CCCGGTCACTGTCCCAACTTTGCGGCTCCCCGCAGAGAGGTGGCACCACC 950
    ||||||||||||||||||||||||||||||||||||||||||||||||||
300 ProGlyAspCysProAsnPheAlaAlaProThrArgAspValAlaProPr 317

951 CTATCAGGGGCTGACCCCATCATTGCCGACAGAGCGCTCCACCTCGAGACCCCA 1000
    |||||||||||||||||||||||||||||||||||||||||||||||||||||
317 oTyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProI 334
```

```
XX
DR   WPI: 1992-043613/06.
DR   N-PSDB; AAQ20973.
XX
PT   New tumour necrosis factor alpha binding protein and polypeptide
PT   - useful in treating cachexia, sepsis and auto immune diseases
PT   e.g. rheumatoid arthritis
XX
PS   Disclosure: Fig 1; 25pp; English.
XX
CC   The amino acid sequence is that of tumour necrosis factor alpha
CC   binding protein which contains the extracellular domain of human TNF
CC   alpha receptor. It is soluble and can be used in the regulation of
CC   TNF-mediated responses by binding and sequestering the cytokine. It
CC   can therefore be used therapeutically to treat disorders such as
CC   cachexia, sepsis and autoimmune diseases, specifically rheumatoid
CC   arthritis.
XX
SQ   Sequence    455 AA.
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alignment_scores:
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        Quality:  2481.00               Length:      455
        Ratio:    5.453                 Gaps:          0
Percent Similarity: 100.000    Percent Identity:  44.560
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alignment_block:
US-09-525-998A-1 x AAR20787 ..

Align seq 1/1 to AAP20787 from 1 to 455

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ID   AAR42197 standard; Protein; 455 AA.
XX
AC   AAR42197;
XX
DT   13-MAY-1994 (first entry)
XX
DE   p55 tumour necrosis factor receptor.
XX
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..21
FT                   /label- Leader peptide.
FT   Domain          183..205
FT                   /label- Transmembrane domain.
XX
PN   EP568925-A.
XX
PD   10-NOV-1993.
XX
PF   29-APR-1993; 93EP-0106981.
XX
PR   03-MAY-1992; 92IL-0101769.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Hrakcbusch C, Wallach D;
XX
DR   WPI; 1993-353057/45.
DR   N-PSDB; AAQ50870.
XX
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
XX
PS   Claim 2; Figure 1; 17pp; English.
XX
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor. This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock. They can also
CC   be used to treat overdoses of exogenous TNF. Specific deletions
CC   include amino acid residues 405-426 from which it was discovered
CC   that amino acids 405-414, or part of them, are essential for the
CC   signalling of the human p55 TNF-R for the cytotoxic effect of TNF
CC   whereas amino acids 415-426 are not essential. Also residues
CC   170-174, 174-179 or both i.e 170-179 were deleted. This region of
CC   amino acids, or part of, when deleted, abolished shedding of the
CC   soluble extracellular forms of the protein.
XX
SQ   Sequence 455 AA;

alignment_scores:
        Quality: 2478.00        Length:       455
          Ratio: 5.446            Gaps:         0
Percent Similarity: 100.000    Percent Identity: 99.560

alignment_block:
US-09-525-998A-1 x AAR42197 ...

Align seq 1/1 to: AAR42197   from: 1   to: 455

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      1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl      17

   51 ...                                                   100
     17 uLeuLeuValGlyLeuTyrProSerGlyValLeuGlyLeuValProHisL      34

  101 ...                                                   150
     34 euGlyAlaArgGluLysArgAspSerValCysProGlnGlyLysTyrIle      50

  151 ...                                                   200
     51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy      67

  201 ...                                                   250
     67 LeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC      84

  251 ...                                                   300
     84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu     100

  301 ...                                                   350
    101 SerCysSerLysCysArgLysGlyMetGlyValGluIleSerSerCy       117

  351 ...                                                   400
    117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH    134

  401 ...                                                   450
    134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu    150

  451 ...                                                   500
    151 AsnAlaThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh    167

  501 ...                                                   550
    167 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA    184

  551 ...                                                   600
    184 ...                                                   200

  601 ...                                                   650
    200 ...                                                   217

  651 ...                                                   700
    217 ...                                                   234

  701 ...                                                   750
    234 ...                                                   250

  751 ...                                                   800
    250 ...                                                   267

  801 ...                                                   850
    267 ...                                                   284

  851 ...                                                   900
    284 ...                                                   300

  901 ...                                                   950
```

```
301 ProGlyAspCysPr:Al:PrcAl:AlaPr:AlaAr:AlaArgGluValAlaP:.Pr 317
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951 CTATCAGGGGGCTGACCCCATCCTTGCGACACAGCCCTCCGCCTCCGACCCCA 1000
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
317 GlyGlnGlyAlaAspProG:cGlnAlaTh:AlaAlaGaAlaSerAspTrpl| 334

1001 TGCCCAACACGCTTCAAAGGTGAAGGACAAGGGCACAAAGTGACAAGAGc 1050
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
334 SerProAsnProLeuGlnGlySerTrpGluAspGluAlaHisLysProGlnSer 350

1051 CTAGAGATCAGGGATGCCCCGGACAGGCCCTGAGCCGGCTGCAGACTAACTTCCC 1100
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
351 LeuAspThrAspProAlaProProAlaTh:AlaVaiGluAsnValPr 367

1101 CCCTCCCGTCCAAGCAATTCCCCCTCCCCTCACCGGCAGGCCACCACC 1150
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
367 ProLeuArgTrpLysGluPr.ValArgAr:LeuGlyLeuSerArgAspHisG 384

1151 AGATCGGATCGGTGAAATCGTAAAACTGTAGGTGTTGTAGGGGAAC 1200
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
384 IuIleAspArgLeuGluLeuGlnAsnGlyArgGlyLeuArgGluAlaCin 400

1201 TACACCATCCTGCCGACGCGGGAGCCCTGGAGCCGGCTCAGTGGCAGCAGGAC 1250
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
401 TyrSerMetLeuAlaThrIrpAIgArgArgThrProArgArgGluAlaGlnTh 417

1251 CCTCCAGCGCTGCTCCGACCCGCCGTCCCGGACAGGCAACCTCCTGGGGTCCC 1300
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
417 rLeuGlnLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGlyCysl 434

1301 TGGAGAAATCGGAAGGAGGGTTTGCACGCTGCTAACTTGCAGGGCCGGCGG 1350
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||
434 euGluAspIleGluGluAlaleuCysGlyProAlaAlaAlaLeuProProAla 450

1351 CCCAGTCTTCTCAGA 1365
     |||||||||||||||
451 ProSerLeuLeuArg 455
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seq_name: AAR51034 standard: Protein: 455 AA.

seq_documentation_block:
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ID   AAR51034 standard; Protein; 455 AA.
XX
AC   AAR51034;
XX
DT   13-MAY-1994 (first entry)
XX
DE   Mutant p55 tumour necrosis factor receptor.
XX
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW   effector protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1..21
FT                   /label= Leader peptide.
FT   Domain          183..205
FT                   /label= Transmembrane domain.
XX
PN   EP568925-A.
XX
PD   10-NOV-1993.
XX
PF   29-APR-1993; 93EP-0106981.
XX
PR   03-MAY-1992; 92IL-0101769.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Brakebusch C, Wallach D;
XX
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DR   WPI; 1993 373377,45.
DR   N-PSDB; AAQ50870.
XX
PT   Modulating activity of tumour necrosis factor receptor using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto immune
PT   disease, septic shock, etc.
XX
PS   Claim 5; Figure 1; 17pp; english.
XX
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor. This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock. They can also
CC   be used to treat conditions of excess of TNF. Specific deletions
CC   include amino acid residues 405-426 from which it was discovered
CC   that amino acids 405-414, or part of them, are essential for the
CC   signalling of the human p55 TNF-R for the cytotoxic effect of TNF
CC   whereas amino acids 415-426 are not essential. Also residues
CC   170-174, 174-179 or both i.e 170-179 were deleted. This region of
CC   amino acids, or part of, when deleted abolished shedding of the
CC   soluble extracellular forms of the protein. This sequence
CC   corresponds to the wild type protein disclosed in AAR42197 except
CC   that alanine at position 197 has been substituted in place of serine.
CC   The substitution inhibits cleavage of the soluble form of the
CC   protein.
XX
SQ   Sequence   455 AA;
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alignment_scores:
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         Quality:  2475.00        Length:       455
         Ratio:       5.440        Gaps:            0
Percent Similarity: 100.000   Percent Identity: 99.341
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alignment_block:
us-09-525-998A-1 x AAR51034

Align seq 1/1 to: AAR51034 from: 1 to: 455

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  1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluGl  17

 51 GCTGGTGCTGGAAATAATAGGCCCAGGGATTATTGGAAACTGGCTACC 100
    |||||||||||||||||||||||||||||||||||||||||||||||||
 17 uLeuLeuValGlyIleIleValProGlyValIleGlyLeuValProHisl  34

101 TAGGGGACAGGGAGAGAAGAAATAGTTGGTGGTGCCAAGGAAAATATAA 150
    |||||||||||||||||||||||||||||||||||||||||||||||||
 34 euGlyAspArgGluGlySerValCysProGlnGlyLysTyrIle  50

151 CACCCTCAAAATAAATTCCATTGGCTGTACCAAGTGCCACAAACGAACCTA 200
    |||||||||||||||||||||||||||||||||||||||||||||||||
 51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy  67

201 CCTGTACAATGGACTGTGAGGCCAGGGAGGAATGGAGTTGAGGGAGT 250
    |||||||||||||||||||||||||||||||||||||||||||||||||
 67 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluCys  84

251 GTGAGAGGCGGTCCTTCACCGCTTCAGAAAACCACCTTCACACTGCCCT 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
 84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100

301 AGTTGCTGCAAATGCCGAAAGGAAAATGGGTCACGTCACGTGCAGATCTTCTTG 350
    |||||||||||||||||||||||||||||||||||||||||||||||||
100 ysArgAspHisCysProGlyProGlyArgAlaArgAlaArgGluValAlaPr 117

351 CACAGTGGAGGGAGAGAGATGGTGGGAGGAAAGAAAGAAACGAGAGGGGC 400
```

```
417  rLeuGluLeuLeuGlyGlyArgValLeuArgAspMetAspLeuLeuGlyGlyCysL  434
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1301 TGGAGGAATGGAGGAG...TTGG...GGGGGGG..........GGGGGGGGGGGGGGG  1350
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
434  euGluAspIleGluGluAlaLeuCysGlyProAlaAlaLeuProProAla  450

1351 CCCAGTCTCTCAGA  1365
     ||||||||||||||
451  ProSerLeuLeuArg  455
```

```
117  sThrValAspArgAspThrValCysGlyCysArgLysArgGlnThrTyrArgH  134
401  ATTATGGGAGTGAAAA...TTTCAGTG...TCAATTGTAG...TGCATC       450
134  isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu      150
451  AATGGCACCGTGCACCTCTCCTGCCAGGACAAACAGAACACCTGTGCCAC     500
151  AsnAlaThrValHisLeuSerCysGlnGlnLysGlnAsnThrValCysTh     167
501  CTGCCCATGCAGGTGTTGTTTAAGACAGAAAACGAGTGTGTCTGTGTAGTA    550
167  rCysHisAlaGlyPheCysLeuArgGluAsnGluCysValSerCysSerA     184
551  ACTGTAAGAAAAGGTGGAGTGCACGAATTGTGCCTACCCCAGAATTGAG      600
184  snCysLysLysArgTrpSerAlaArgIleCysProThrProGluLeuGlu     200
601  AAGGTTAAGGGCACTGCAGGACTTCAGGACCACACAGTGTCTTGCCCCTGGT   650
201  AsnValLysGlyThrAlaGlyLeuGlnThrThrValLeuLeuProLeuVa     217
651  CATTTCTTTGGTCTTTGCCTTTTATCCCTCTCATTGGTTTAAVGT          700
217  IleProPhePheGlyLeuCysLeuLeuGlyAlaLeuLeuPheIleGlyLeuMet    234
701  ATCGCTACCAACGGTGGAAGTCCAAGCTTCACTGTTGTTGTGGGAAA       750
234  yrArgTyrCThrArgTrpCThrArgTrpLysSerLTrpSerIleCysValCysGlyLys  250
751  TCGACACCTGAAAAAGAGGGGCAGCTTGAAGGAACTACTACTAAGCCCCT    800
251  SerThrProGluLysGluGlyGluLeuGluGluLeuLeuThrThrLysProLe  267
801  GCCCCCAAAACTCAAGTTCACTCCCACTCCCAGGCTTCACCCCACCCTCG    850
267  uAlaProAsnProSerPheSerProThrProGlyLeuProThrProThrLeuG    284
851  GCTTCAGTCGCGTGCAGTCCAAGTCAGTCACCTGCAGTGTCCAGGTTATAG   900
284  lyPheSerProValProSerThrPheThrSerSerThrTyrThr          300
901  CCCGGCGACTCTCCCAACTTGGGCGTCCGGCATGAGAGTGGAGGCACC      950
301  ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPro     317
951  CTATCAGGGGGCTGACCCCATCCTTGGCACATGCTTGGGCTGGCTGACCCA   1000
317  oLTyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuCysLeuAlaSerAspProI  334
1001 TCCCAAGCCCTTCAAAATGGAGGAGAGGGAGAGGACAAAGGCAGAC        1050
334  leProAsnProLeuGlnLysTrpGluAspSerArgAlaHisLysProGlnSer   350
1051 CTAGCACTGCAGCCCCCCGCCTAGTCCCCGTGGAGAAGCGTGCC          1100
351  LeuAspThrAspAspProAlaThrLeuTyrAlaValGluAsnValPr        367
1101 CCCGTTGCGGTGGAAGGAATCCGTGCGGGCGCCTAGGCTGAGCGCACCACG    1150
367  oProLeuArgTrpLysGlyProHisValArgArgLeuGlyLeuSerAspHisG    384
1151 AGATCGATGAGTTAAAGTAAAAGAGACTGGTGGAGGAGGAA...GGCAA     1200
384  luIleAspArgLeuLeuLysSerGlnHisAsnGlyArgCysIleuAlaGln    400
1201 TACAGTATTCTGCAGGCCCGAGCGCGCCACGCCGGCGCCCGAGCCCAC      1250
401  TyrSerMetLeuAlaThrIleProArgArgAlaIleProProArgArgGluAlaTh  417
1251 GCTCGGAGTTGTGCGGCGGCCCTCGCACACATGGAGCATGGTGGGCGGCGCCC  1300
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